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GenCore version 4.5

OM nucleic - nucleic search, using sw model
Run on: December 3, 2000, 10:15:10 : Search time 10069.4 Seconds
(without alignments) 3787.874 Million cell updates/sec

Title: US-09-227-881-3
perfect score: 6169
sequence: 1atctttgttcagttaccc.....cttggccctccatgtca 6169
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 7189864 seqs, 3091403243 residues
Total number of hits satisfying chosen parameters: 14379728
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_est4:*

5: gb_est5:*

6: gb_est6:*

7: gb_est7:*

8: gb_est8:*

9: gb_est9:*

10: gb_est10:*

11: gb_est11:*

12: gb_est12:*

13: gb_est13:*

14: gb_est14:*

15: gb_est15:*

16: gb_est16:*

17: gb_est17:*

18: gb_est18:*

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42: em_esttun1:*

43: em_esthun1:*

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45: em_esthun3:*

46: em_esthun4:*

47: em_esthun5:*

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63: em_estin1:*

64: em_estin2:*

65: em_estin3:*

66: em_estin4:*

67: em_gestm:*

68: em_estov1:*

69: em_estov2:*

70: em_estp1:*

71: em_estp12:*

72: em_estp13:*

73: em_estp14:*

74: em_estp15:*

75: em_estr01:*

76: em_estr02:*

77: em_estr03:*

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79: em_estr05:*

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88: em_gss1:*

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91: em_gss4:*

92: em_gss1:*

93: em_gss2:*

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108: em_gss17:*

109: em_gss18:*

110: em_gss19:*

111: em_gss20:*

112: em_gss21:*

113: em_gss22:*

114: em_gss23:*

115: em_gss24:*

116: em_gss5:*

Locus A0057239 660 bp DNA
Definition CIT-HSP-2340D14.TR CIT-HSP Homo sapiens genomic clone 2340D14, DNA
Accession A0057239
Version A0057239.1 GI:3353765
Keywords GSS
Source Homo sapiens
Organism Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammal; Eutheria; Primates; Catarhini; Hominidae; Homo.
1 (bases 1 to 660)
Reference Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Sub, E., Wible, C., Shizuya, H.,
Simon, M. and Venter, J.C.
Title Use of a random BAC End Sequence Database for Sequence-Ready Map
Journal Building (1998)
Comment Unpublished (1998)
Other GSS: CIT-HSP-2340D14.TP

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	180.8	2.9	660	88	AQ057239 CIT-HSP-2	
C	2	179.8	2.9	539	96	AQ379787 RPCI-11-15
C	3	179	2.9	645	100	AQ636457 RPCI-11-4
C	4	179	2.9	678	96	AQ387027 RPCI-11-15
C	5	178.4	2.9	537	25	AQ978041 EST390150
C	6	177.6	2.9	516	91	AQ112451 CIT-HSP-2
C	7	177.4	2.9	577	91	AQ253899 CIBR-E1-
C	8	177.2	2.9	548	11	A1583291 tt56902.x
C	9	176.6	2.9	434	90	AQ194335 RPCI-11-58
10	176.6	2.9	591	25	AW979191 EST391301	
11	176	2.9	521	21	AW213360	
12	176	2.9	521	21	AW213360	
13	175.8	2.8	589	91	AQ283440	
C	14	175.4	2.8	386	98	AQ474222 CIBR-E1-
C	15	175.2	2.8	711	97	AQ15030 RPCI-11-2
16	175	2.8	388	19	AW059227 cr41h09.x	
17	175	2.8	421	23	AW674631 bbl1a1.x	
C	18	175	2.8	447	24	AW20784 RC2-ST030
19	175	2.8	454	12	A1634187	
20	175	2.8	474	10	A1457313	
21	175	2.8	527	11	A1523813 t99qd09.x	
22	174.8	2.8	432	9	A1330018 qn47c06.x	
23	174.8	2.8	435	9	A1310992 qn47c06.x	
24	174.6	2.8	424	10	A1431513 th45f04.x	
25	174.6	2.8	677	110	B66612 CIT-HSP-201	
C	26	174.2	2.8	342	6	AQ846233 oe0801.s
C	27	173.8	2.8	460	110	B15692 345Nc.TP.CI
C	28	173.8	2.8	565	25	AW553220 EST365290
C	29	173.8	2.8	368	21	AW720385 xp74-f06.x
C	30	173.6	2.8	374	37	F33684 RSPD3531.H
C	31	173.4	2.8	384	7	AQ852029 o146604.s
C	32	173.4	2.8	427	5	AQ550989 n_j35612.s
C	33	173.4	2.8	436	88	AQ21084 CIT-HSP-2
C	34	173.4	2.8	486	8	A1049955 an38c01.x
C	35	173.4	2.8	642	110	B59854 CIT-HSP-345
C	36	173.4	2.8	836	102	AQ781745 HS3122_A
C	37	173.2	2.8	413	10	A1355246 qt4b406.x
C	38	173.2	2.8	430	13	A185905 wmp3c01.x
C	39	173.2	2.8	508	100	AQ632598 RPCI-11-4
C	40	173.2	2.8	784	101	AQ3738890 HS5382_B
C	41	172.8	2.8	496	4	AQ486819 ab19c10.x
C	42	172.8	2.8	624	96	AQ373399 RPCI-11-15
C	43	172.6	2.8	300	7	AQ937809 nw8902.s
C	44	172.4	2.8	10	A1417469 th3h09.x	
C	45	172.4	2.8	439	14	A1961983 wt4ta12.x

ALIGNMENTS

ACCESSION	AQ387027	RESULT	5
VERSION	AQ387027.1	GI	4358050
KEYWORDS	GSS.	LOCUS	AW978041
SOURCE	human.	DEFINITION	537 bp mRNA
ORGANISM	Homo sapiens	ACCESSION	EST390150
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	COMMENT	DEFINITION	MAGE resequences, MAGO Homo sapiens cDNA, mRNA sequence.
1 (bases 1 to 678)	1 (bases 1 to 537)	VERSION	AW978041.1
Zhao,S., Adams,M.D., Nieman,W., Malek,J., de Jong,P. and Venter,J.C.	1 (bases 1 to 537)	ACCESSION	GI:8169303
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building	REFERENCE	ORGANISM	Homo sapiens
Unpublished (1997)	1 (bases 1 to 537)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
Other GSS: RPCI-11-153C12.TV	Hege,P., Oi,R., Abernathy,K., Dharap,S., Gaspari,R., Gay,C., Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.		
Contact: Shaying Zhao, William Nieman, Mark Adams	COMMENT	TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
Department of Eukaryotic Genomics	Unpublished (2000)	JOURNAL	Unpublished (2000)
The Institute for Genomic Research	Contact: John Quackenbush	COMMENT	Contact: John Quackenbush
9712 Medical Center Dr., Rockville, MD 20850	9712 Medical Center Dr., Rockville, MD 20850, USA	FEATURES	Location/Qualifiers
Tel: 301 838 0200	Tel: 301 838 3528	source	1..537
Fax: 301 838 0208	Fax: 301 838 0208	source	1..537
Email: hbo@jgr.org	Email: John@jgr.org	source	1..537
Clones are derived from the human BAC library RPCI-11. For BAC library availability, Please contact Pieter de Jong (pieter@jgr.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (http://www.ingenuity.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html	source	1..537	
Seq primer: SP6	Seq primer: Forward.	source	1..537
Class: BAC ends.		source	1..537
FEATURES	Location/Qualifiers	source	1..537
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1..578		source	1..537
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/db_xref="taxon:9606"	/db_xref="taxon:9606"	source	1..537
/clone="RPCI-11-153C12"	/clone="RPCI-11-153C12"	source	1..537
/clone_id="RPCI-11-11"	/clone_id="RPCI-11-11"	source	1..537
/sex="Male"	/sex="Male"	source	1..537
/cell_type="Lymphocytes"	/cell_type="Lymphocytes"	source	1..537
/note="vector: PBACE3.6; site_1: ECORI; site_2: ECORI; RPCI1 Human Male BAC Library"	/note="vector: PBACE3.6; site_1: ECORI; site_2: ECORI; RPCI1 Human Male BAC Library"	source	1..537
BASE COUNT	210 a 151 c 171 g 146 t	source	1..537
ORIGIN		source	1..537
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VERSION	A1582291.1	GI:4569188	DEFINITION	RPCI-11-58F5.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-58F5, DNA sequence.
KEYWORDS	EST.		ACCESSION	RP009435.
SOURCE	human.		VERSION	AQ19935.1
ORGANISM	Homo sapiens		KEYWORDS	GSS.
REFERENCE	1 (bases 1 to 548)		ORGANISM	Homo sapiens
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL	Unpublished (1997)		TITLE	Unpublished (1998)
COMMENT	Contact: Robert.Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov		COMMENT	Use of human BAC End Sequences for Sequence-Ready Map Building
TISSUE	Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,		JOURNAL	Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
PROCUREMENT	M.D., Ph.D.		CONTACT	Other GSS: RPCI-11-58F5.TK
CNA	Library Preparation: David B. Kitzman, Ph.D.		DEPARTMENT	Department of Eukaryotic Genomics
LIBRARY	Library Arrayed by: Greg Lennon, Ph.D.		PI	9712 Medical Center Dr., Rockville, MD 20850, USA
SEQUENCING	DNA Sequencing by: Washington University Genome Sequencing Center		TELEPHONE	301 838 0200
CENTER	Clone distribution: NCI-CGAP clone distribution information can be found through the T.M.A.G.E. Consortium/LNLT at: www-bio-lnl.gov/bbpr/image/image.html		FAX	301 838 0208
INSTRUMENT	Insert Length: 664 Std Error: 0.00		EMAIL	madams@tigr.org
POLY-A-NO.	Seq primer: -400P from Gibco High quality sequence stop: 464		CLONES	Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pjeter@joung-med.buffalo.edu). Clones may be purchased from BAC/PAC Resources (http://bacpac.med.buffalo.edu/Ordering) or from Research Genetics (http://www.resres.com). BAC end search page: http://www.tigr.org/rtdb/hungen/bac_end_search/bac_end_search.html
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